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1/6

1/0	
ATGTCCATGA ACTGCTGAGT GGATAAACAG CACGGGATAT CTCTGTCTAA AGGAATATTA CTACACCAGG AAAAGGACAC ATTCGACAAC AGGAAAGGAG CCTGTCACAG AAAACCACAG TGTCCTGTGC ATGTGACATT TCGCC	-96 -46 -1
ATG GGA AAC AAC TGT TAC AAC GTG GTG GTC ATT GTG CTG CTA Met Gly Asn Asn Cys Tyr Asn Val Val Ile Val Leu Leu Leu	45
GTG GGC TGT GAG AAG GTG GGA GCC GTG CAG AAC TCC TGT GAT AAC Val Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn	90
TGT CAG CCT GGT ACT TTC TGC AGA AAA TAC AAT CCA GTC TGC AAG Cys Gln Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys . H4-1BB FI	135
AGC TGC CCT CCA AGT ACC TTC TCC AGC ATA GGT GGA CAG CCG AAC Ser Cys Pro Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn H4-1BB FII	180
TGT AAC ATC TGC AGA GTG TGT GCA GGC TAT TTC AGG TTC AAG AAG Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys	225
TTT TGC TCC TCT ACC CAC AAC GCG GAG TGT GAG TGC ATT GAA GGA Phe Cys Ser Ser Thr His Asn Ala Glu Cys Glu Cys Ile Glu Gly	270
TTC CAT TGC TTG GGG CCA CAG TGC ACC AGA TGT GAA AAG GAC TGC Phe His Cys Leu Gly Pro Gln Cys Thr Arg Cys Glu Lys Asp Cys	315
AGG CCT GGC CAG GAG CTA ACG AAG CAG GGT TGC AAA ACC TGT AGC Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys Thr Cys Ser . H4-1BB RI .	360
TTG GGA ACA TTT AAT GAC CAG AAC GGT ACT GGC GTC TGT CGA CCC Leu Gly Thr Phe Asn Asp Gln Asn Gly Thr Gly Val Cys Arg Pro H4-1BB RII	405
TGG ACG AAC TGC TCT CTA GAC GGA AGG TCT GTG CTT AAG ACC GGG Trp Thr Asn Cys Ser Leu Asp Gly Arg Ser Val Leu Lys Thr Gly	450
ACC ACG GAG AAG GAC GTG GTG TGT GGA CCC CCT GTG GTG AGC TTC Thr Thr Glu Lys Asp Val Val Cys Gly Pro Pro Val Val Ser Phe .	495
TCT CCC AGT ACC ACC ATT TCT GTG ACT CCA GAG GGA GGA CCA GGA Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu Gly Gly Pro Gly	540
GGG CAC TCC TTG CAG GTC CTT ACC TTG TTC CTG GCG CTG ACA TCG Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala Leu Thr Ser	585
GCT TTG CTG CTG GCC CTG ATC TTC ATT ACT CTC CTG TTC TCT GTG Ala Leu Leu Ala Leu Ile Phe Ile Thr Leu Leu Phe Ser Val	630



2/6

	G ATC AGG A p Ile Arg L								675
	G ACC ACT G s Thr Thr G								720
	T CCA CAG G s Pro Gln G								765
CTG TGA Leu									771
TGTACTATCC	TAGGAGATGT	GTGGGC	CGAA A	ACCGAGA	AAGC	ACTA	AGGA	CCC	821
	TGGAACAGCA								871
	TGATGTGTGG								921
	TGTCTTTACC								971
	AGTGTTTTGC								1021
	CTCCTGATGC								1071
	TGGAGTTATG								1121
	GTCTTCTTAT								1171
	GAATTGTAGA								1221
	TTGTTGATAC								1271
GTTACCAGGT	ATAAGACTCT	CCACAM	mmma (AAGTCA <i>E</i>	ACCT	AGAG	J.T.G.T.C	CIG	1321 1371
ACACACACAC	ACGTTTATAC	TACCTA	CTIA (℧℄℄℧Å℧Å	LV TUT	CTA	CTC	ノみし	$\frac{1371}{1421}$
TAATGGGATA									1471
GGTGACAGAC	TACCCCTTCT	GGGTAC	GTAG (CCACACA		CCLL	rccci	2022 2022	1521
GTCTAAAACT	CCCCTTAGAA	GTCTCG	TCAA (GTTCCCC	GAC	GAAG	FAGG	ACA	1571
GAGGAGACAC									1621
TCGTGACACT	CCACCCCTTG	TGGACA	CTTG A	AGTGTCA	TCC	TTGC	CGCC	GGA	1671
	GTACCCGTCT								1721
GCTACGAGAA									1771
TTTAATCTCA	CAAGTTTCGT	CCGGGC'	TCGG (CGGACCI	ATG	GCGT	CGA	CC	1821
TTATTACCTT									1871
GGTACTAATT	CTCCCTGCCG	GCCCCC	GTAA (GCATAAC	CGCG	GCGI	ATCT	CCA	1921
CTTTAAGAAC	CTGGCCGCGT	TCTGCC'	TGGT (CTCGCTT	TCG	TAAZ	ACGG:	ГТС	1971
TTACAAAAGT									2021
ATGGCAGCAT									2071
AATAAGGGTA	CTGGGCGGCC	CGTCGA	AGGC (CCTTTG	STTT	CAG	AAAC	CCA	2121
AGGCCCCCT					rgcc	GGT	ACGT	GGT	2171
GGTGGGTGCC	TTAGCTCTTT	CTCGAT.	AGTT A	AGAC					2205

3/6

human homologue of mouse 4-1bb h4-1bb Length 838

1	AATCAGCTTT	GCTAGTATCA	TACCTGTGCC	AGATTTCATC	ATGGGAAACA
51	GCTGTTACAA	CATAGTAGCC	ACTCTGTTGC	TGGTCCTCAA	CTTTGAGAGG
101	ACAAGATCAT	TGCAGGATCC	TTGTAGTAAC	TGCCCAGCTG	GTACATTCTG
151	TGATAATAAC	AGGAATCAGA	TTTGCAGTCC	CTGTCCTCCA	AATAGTTTCT
201	CCAGCGCAGG	TGGACAAAGG	ACCTGTGACA	TATGCAGGCA	GTGTAAAGGT
251	GTTTTCAGGA	CCAGGAAGGA	GTGTTCCTCC	ACCAGCAATG	CAGAGTGTGA
301	CTGCACTCCA	GGGTTTCACT	GCCTGGGGGC	AGGATGCAGC	ATGTGTGAAC
351	AGGATTGTAA	ACAAGGTCAA	GAACTGACAA	AAAAAGGTTG	TAAAGACTGT
401	TGCTTTGGGA	CATTTAACGA	TCAGAAACGT	GGCATCTGTC	GACCCTGGAC
451	AAACTGTTCT	TTGGATGGAA	AGTCTGTGCT	TGTGAATGGG	ACGAAGGAGA
501	GGGACGTGGT	CTGTGGACCA	TCTCCAGCTG	ACCTCTCTCC	GGGAGCATCC
551	TCTGTGACCC	CGCCTGCCCC	TGCGAGAGAG	CCAGGACACT	CTCCGCAGAT
601	CATCTCCTTC	TTTCTTGCGC	TGACGTCGAC	TGCGTTGCTC	TTCCTGCTGT
651	TCTTCCTCAC	GCTCCGTTTC	TCTGTTGTTA	AACGGGGCAG	AAAGAAACTC
701	CTGTATATAT	TCAAACAACC	ATTTATGAGA	CCAGTACAAA	CTACTCAAGA
751	GGAAGATGGC	TGTAGCTGCC	GATTTCCAGA	AGAAGAAGAA	GGAGGATGTG
801	AACTGTGAAA	TGGAAGTCAA	TAGGGCTGTT	GGGACTTT	

Fig. 2A

1	MGNSCYNIVA	TLLLVLNFER	TRSLODECSN	CPAGTECDNN	RNOTCSPCPP
$5\overline{1}$		TCDICROCKG	~		~
101	MCEQDCKQGQ				
151	TKERDVVCGP				
201		SVVKRGRKKL		~	
251	GGCEL	DVVIIIGITITI	HITTRQLIM	IVQIIQEEDG	COCKLIBBEE

Fig.2B

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Hand)

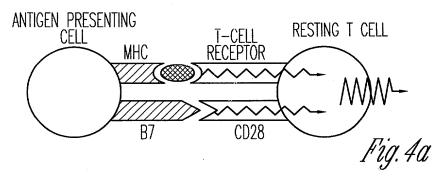
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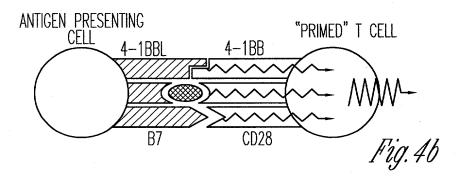
Fig.3b

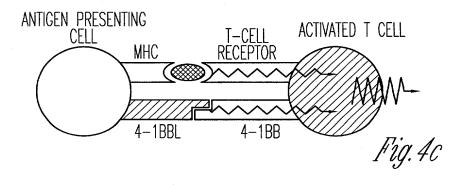
5/6



NORMAL T CELL ACTIVATION PATHWAY







6/6

BLOCKING STEPS IN T-CELL ACTIVATION PATHWAY

